

\$%^STN;HighlightOn= ***;HighlightOff=*** ;

Connecting via Winsock to STN

Welcome to STN International! Enter x:x

LOGINID:SSSPTAGSE1646

PASSWORD:

TERMINAL (ENTER 1, 2, 3, OR ?):2

* * * * * Welcome to STN International * * * * *

NEWS 1 Web Page URLs for STN Seminar Schedule - N. America
NEWS 2 "Ask CAS" for self-help around the clock
NEWS 3 FEB 25 CA/CAPLUS - Russian Agency for Patents and Trademarks
(ROSPATENT) added to list of core patent offices covered
NEWS 4 FEB 28 PATDPAFULL - New display fields provide for legal status
data from INPADOC
NEWS 5 FEB 28 BABS - Current-awareness alerts (SDIs) available
NEWS 6 FEB 28 MEDLINE/LMEDLINE reloaded
NEWS 7 MAR 02 GBFULL: New full-text patent database on STN
NEWS 8 MAR 03 REGISTRY/ZREGISTRY - Sequence annotations enhanced
NEWS 9 MAR 03 MEDLINE file segment of TOXCENTER reloaded
NEWS 10 MAR 22 KOREAPAT now updated monthly; patent information enhanced
NEWS 11 MAR 22 Original IDE display format returns to REGISTRY/ZREGISTRY
NEWS 12 MAR 22 PATDPASPC - New patent database available
NEWS 13 MAR 22 REGISTRY/ZREGISTRY enhanced with experimental property tags
NEWS 14 APR 04 EPFULL enhanced with additional patent information and new
fields
NEWS 15 APR 04 EMBASE - Database reloaded and enhanced
NEWS 16 APR 18 New CAS Information Use Policies available online
NEWS 17 APR 25 Patent searching, including current-awareness alerts (SDIs),
based on application date in CA/Caplus and USPATFULL/USPAT2
may be affected by a change in filing date for U.S.
applications.
NEWS 18 APR 28 Improved searching of U.S. Patent Classifications for
U.S. patent records in CA/Caplus
NEWS 19 MAY 23 GBFULL enhanced with patent drawing images
NEWS 20 MAY 23 REGISTRY has been enhanced with source information from
CHEMCATS
NEWS 21 MAY 26 STN User Update to be held June 6 and June 7 at the SLA 2005
Annual Conference
NEWS 22 JUN 06 STN Patent Forums to be held in June 2005
NEWS 23 JUN 06 The Analysis Edition of STN Express with Discover!
(Version 8.0 for Windows) now available

NEWS EXPRESS JANUARY 10 CURRENT WINDOWS VERSION IS V7.01a, CURRENT
MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP),
AND CURRENT DISCOVER FILE IS DATED 10 JANUARY 2005

NEWS HOURS STN Operating Hours Plus Help Desk Availability
NEWS INTER General Internet Information
NEWS LOGIN Welcome Banner and News Items
NEWS PHONE Direct Dial and Telecommunication Network Access to STN
NEWS WWW CAS World Wide Web Site (general information)

Enter NEWS followed by the item number or name to see news on that
specific topic.

All use of STN is subject to the provisions of the STN Customer
agreement. Please note that this agreement limits use to scientific
research. Use for software development or design or implementation
of commercial gateways or other similar uses is prohibited and may
result in loss of user privileges and other penalties.

* * * * * STN Columbus * * * * *

FILE 'HOME' ENTERED AT 15:19:46 ON 07 JUN 2005

=> FILE BIOSIS, CAPLUS
COST IN U.S. DOLLARS

SINCE FILE	TOTAL
ENTRY	SESSION
0.63	0.63

FULL ESTIMATED COST

FILE 'BIOSIS' ENTERED AT 15:21:47 ON 07 JUN 2005
Copyright (c) 2005 The Thomson Corporation

FILE 'CAPLUS' ENTERED AT 15:21:47 ON 07 JUN 2005
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.
COPYRIGHT (C) 2005 AMERICAN CHEMICAL SOCIETY (ACS)

=> S CXCR3 AND (Mig OR IP-10)
L1 581 CXCR3 AND (MIG OR IP-10)

=> dup rem
ENTER L# LIST OR (END):L1
PROCESSING COMPLETED FOR L1
L2 421 DUP REM L1 (160 DUPLICATES REMOVED)

SINCE FILE	TOTAL
ENTRY	SESSION
14.51	15.14

SESSION WILL BE HELD FOR 60 MINUTES
STN INTERNATIONAL SESSION SUSPENDED AT 15:28:33 ON 07 JUN 2005

Connecting via Winsock to STN

Welcome to STN International! Enter x:x

LOGINID:SSSPTAGSE1646

PASSWORD:
* * * * * RECONNECTED TO STN INTERNATIONAL * * * * *
SESSION RESUMED IN FILE 'BIOSIS, CAPLUS' AT 15:30:33 ON 07 JUN 2005
FILE 'BIOSIS' ENTERED AT 15:30:33 ON 07 JUN 2005
Copyright (c) 2005 The Thomson Corporation
FILE 'CAPLUS' ENTERED AT 15:30:33 ON 07 JUN 2005
COPYRIGHT (C) 2005 AMERICAN CHEMICAL SOCIETY (ACS)

SINCE FILE	TOTAL
ENTRY	SESSION
14.51	15.14

=> d his

(FILE 'HOME' ENTERED AT 15:19:46 ON 07 JUN 2005)

FILE 'BIOSIS, CAPLUS' ENTERED AT 15:21:47 ON 07 JUN 2005
L1 581 S CXCR3 AND (MIG OR IP-10)
L2 421 DUP REM L1 (160 DUPLICATES REMOVED)

=> s l2 py<2000
MISSING OPERATOR L2 PY<2000
The search profile that was entered contains terms or
nested terms that are not separated by a logical operator.

=> s l2 and py<2000
L3 49 L2 AND PY<2000

=> s l2 and py=<2000
L4 81 L2 AND PY=<2000

=> d 14 ti 1-25

- L4 ANSWER 1 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
TI Effect of IL-8 produced by oral squamous cell carcinoma cell lines on proliferation and chemotaxis of endothelial cells.
- L4 ANSWER 2 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
TI Groatpha/KC, a ligand for chemokine receptor CXCR2, can be a potent trigger for neuronal ERK1/2, PI-3 kinase pathways and for tau hyperphosphorylation in vitro: a role in Alzheimer's disease?.
- L4 ANSWER 3 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
TI High expression of chemokines Interferon-gamma Inducible Protein of 10 kDa (***IP*** - ***10***), Monokine induced by Interferon-gamma (***Mig***) and of their receptor (***CXCR3***) in different renal diseases.
- L4 ANSWER 4 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
TI The role of ***IP*** - ***10*** and ***CXCR3*** in the pathogenesis of type I diabetes mellitus.
- L4 ANSWER 5 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
TI Chemokines and chemokine receptors in altered peptide ligand modulation of experimental allergic encephalomyelitis.
- L4 ANSWER 6 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
TI Stability of chemokine receptor expression and plasma chemokine levels in healthy individuals.
- L4 ANSWER 7 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
TI Requirement of the chemokine receptor ***CXCR3*** for acute allograft rejection.
- L4 ANSWER 8 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
TI Modulation of experimental autoimmune encephalomyelitis: Effect of altered peptide ligand on chemokine and chemokine receptor expression.
- L4 ANSWER 9 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
TI The chemokine/chemokine-receptor family: Potential and progress for therapeutic intervention.
- L4 ANSWER 10 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
TI Selective lymphocyte expression of ***CXCR3*** and its association with inflammatory diseases.
- L4 ANSWER 11 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
TI Differential expression and responsiveness of chemokine receptors (CXCR1-3) by human microvascular endothelial cells and umbilical vein endothelial cells.
- L4 ANSWER 12 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
TI CXC chemokines ***IP*** - ***10*** and ***Mig*** expression and direct migration of pulmonary CD8+/ ***CXCR3*** + T cells in the lungs of patients with HIV infection and T-cell alveolitis.
- L4 ANSWER 13 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
TI The T cell chemokine receptor ***CXCR3*** is highly expressed in the early stages of mycosis fungoides.
- L4 ANSWER 14 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
TI Expression of ***IP*** - ***10*** and its receptor ***CXCR3*** in hepatic stellate cells identifies a novel autocrine and paracrine system.
- L4 ANSWER 15 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN

TI The neutrophil chemoattractant GCP-2 selectively antagonizes the interaction of IP10 with ***CXCR3*** .

L4 ANSWER 16 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN

TI Differences in receptor binding and signalling-transducing properites of ***IP*** - ***10*** , ***MIG*** and I-TAC revealed through the characterization of amino-terminal truncation mutants of ***CXCR3*** .

L4 ANSWER 17 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN

TI Targeted disruption of the ***MIG*** gene reveals a role for ***MIG*** in antibody production.

L4 ANSWER 18 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN

TI CXC chemokine receptor 3 expression on CD34+ hematopoietic progenitors from human cord blood induced by granulocyte-macrophage colony-stimulating factor: Chemotaxis and adhesion induced by its ligands, interferon gamma-inducible protein 10 and monokine induced by interferon gamma.

L4 ANSWER 19 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN

TI Expression of the chemokine receptor ***CXCR3*** on neurons and the elevated expression of its ligand ***IP*** - ***10*** in reactive astrocytes: In vitro ERK1/2 activation and role in Alzheimer's disease.

L4 ANSWER 20 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN

TI The CXC chemokines gamma interferon (IFN-gamma)-inducible protein 10 and monokine induced by IFN-gamma are released during severe melioidosis.

L4 ANSWER 21 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN

TI Expression pattern of T-cell-associated chemokine receptors and their chemokines correlates with specific subtypes of T-cell non-Hodgkin lymphoma.

L4 ANSWER 22 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN

TI Identification and molecular characterization of rat ***CXCR3*** : Receptor expression and interferon-inducible protein-10 binding are increased in focal stroke.

L4 ANSWER 23 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN

TI Expression of the interferon-gamma-inducible chemokines ***IP*** - ***10*** and ***Mig*** and their receptor, ***CXCR3*** , in multiple sclerosis lesions.

L4 ANSWER 24 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN

TI Expression of ***IP*** - ***10*** and its receptor ***CXCR3*** in hepatic stellate cells identifies a novel autocrine and paracrine system.

L4 ANSWER 25 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN

TI Differential expression of three T lymphocyte-activating CXC chemokines by human atheroma-associated cells.

=> d l4 ti 26-81

L4 ANSWER 26 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN

TI Lack of chemokine receptor CCR1 enhances Th1 responses and glomerular injury during nephrotoxic nephritis.

L4 ANSWER 27 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN

TI The chemokine receptor ***CXCR3*** is expressed on malignant B cells

and mediates chemotaxis.

- L4 ANSWER 28 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on
STN
TI Interferon (IFN)-gamma regulated production of chemoattractants specific
for CD4+ memory T cells by human intestinal epithelial cells.
- L4 ANSWER 29 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on
STN
TI IL-4 enhances IFN-gamma- and TNF-alpha-induced keratinocyte expression of
IP - ***10*** , ***Mig*** and I-TAC chemokines targeting
CXCR3 + T cells to the skin.
- L4 ANSWER 30 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on
STN
TI Internalization of ***CXCR3*** on activated T cells following contact
with IFNg-activated human endothelial cells: Differential effects of
I-TAC, ***Mig*** , and I-TAC.
- L4 ANSWER 31 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on
STN
TI The chemokine receptor ***CXCR3*** is expressed in a subset of B-cell
lymphomas and is a marker of B-cell chronic lymphocytic leukemia.
- L4 ANSWER 32 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on
STN
TI T cell attractant chemokine expression initiates lacrimal gland
destruction in nonobese diabetic mice.
- L4 ANSWER 33 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on
STN
TI Binding to chemokine receptors CXCR2 and ***CXCR3*** by their
respective ligands KC and ***IP*** - ***10*** induces the activation
of MAP kinase (ERK1/2) in mouse cortical neurons.
- L4 ANSWER 34 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on
STN
TI Role for interactions between ***IP*** - ***10*** / ***Mig*** and
CXCR3 in proliferative glomerulonephritis.
- L4 ANSWER 35 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on
STN
TI The expression pattern of T cell-associated chemokine receptors correlates
with specific subtypes of T cell lymphoma.
- L4 ANSWER 36 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on
STN
TI Chemokine receptors involvement in B-cell lymphoproliferative disorders.
- L4 ANSWER 37 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on
STN
TI Structure and function of the murine chemokine receptor ***CXCR3*** .
- L4 ANSWER 38 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on
STN
TI The ***CXCR3*** activating chemokines ***IP*** - ***10*** ,
Mig , and IP-9 are expressed in allergic but not in irritant patch
test reactions.
- L4 ANSWER 39 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on
STN
TI ***IP*** - ***10*** and ***Mig*** , chemoattractants for Th1
cells, and their receptor (***CXCR3***) are highly expressed in
rheumatoid arthritis synovium.
- L4 ANSWER 40 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on
STN
TI SLC/Exodus2/6Ckine/TCA4 induces chemotaxis of hematopoietic progenitor
cells: Differential activity of ligands of CCR7, ***CXCR3*** , or CXCR4
in chemotaxis vs. suppression of progenitor proliferation.
- L4 ANSWER 41 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on

STN
 TI Molecular characterization of a human chemokine receptor that is activated by ***IP*** - ***10*** and ***MIG*** .

L4 ANSWER 42 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
 TI RANTES and ***IP*** - ***10*** as well as their receptors CCR1 and ***CXCR3*** predict acute rejection in human cardiac allografts.

L4 ANSWER 43 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
 TI Cellular and humoral mechanisms of vascularized allograft rejection induced by indirect recognition of donor MHC allopeptides.

L4 ANSWER 44 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
 TI CCR5+ and ***CXCR3*** + T cells are increased in multiple sclerosis and their ligands MIP-1alpha and ***IP*** - ***10*** are expressed in demyelinating brain lesions.

L4 ANSWER 45 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
 TI Expression and function of CXC and CC chemokines in human malignant liver tumors: A role for human monokine induced by gamma-interferon in lymphocyte recruitment to hepatocellular carcinoma.

L4 ANSWER 46 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
 TI Effects of interferon-gamma-inducible protein (***IP*** - ***10***) and stromal cell-derived factor-1 (SDF-1alpha) on jurkat cells by differential display.

L4 ANSWER 47 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
 TI T cells expressing Th1 associated chemokine receptors CCR5 and ***CXCR3*** are increased in multiple sclerosis, produce high levels of IFN-gamma and their ligands MIP-1alpha and ***IP*** - ***10*** are expressed in demyelinating brain lesions.

L4 ANSWER 48 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
 TI Human IP-9: A keratinocyte-derived high affinity CXC-chemokine ligand for the ***IP*** - ***10*** / ***Mig*** receptor (***CXCR3***).

L4 ANSWER 49 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
 TI Expression of specific chemokines and chemokine receptors in the central nervous system of multiple sclerosis patients.

L4 ANSWER 50 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
 TI Chemokines/chemokine receptors in the central nervous system and Alzheimer's disease.

L4 ANSWER 51 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
 TI Constitutive expression of chemokine receptor ***CXCR3*** on neurons of CNS and elevated expression of ***IP*** - ***10*** in reactive astrocytes of Alzheimer's disease brains.

L4 ANSWER 52 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
 TI Lymphocyte-specific chemokine receptor ***CXCR3*** : Regulation, chemokine binding and gene localization.

L4 ANSWER 53 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
 TI ***IP*** - ***10*** , ***Mig*** and ***CXCR3*** expression in multiple sclerosis at different stages of lesion development.

L4 ANSWER 54 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN

TI Expression of the chemokine receptor ***CXCR3*** and its ligand, ***Ip*** - ***10*** , in macaques with experimental allergic encephalitis.

L4 ANSWER 55 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN

TI Binding and functional properties of recombinant and endogenous ***CXCR3*** chemokine receptors.

L4 ANSWER 56 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN

TI Interferon-inducible T cell alpha chemoattractant (I-TAC): A novel non-ELR CXC chemokine with potent activity on activated T cells through selective high affinity binding to ***CXCR3*** .

L4 ANSWER 57 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN

TI Molecular cloning of a novel chemokine receptor-like gene from early stage chick embryos.

L4 ANSWER 58 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN

TI The chemokine receptor ***CXCR3*** mediates rapid and shear-resistant adhesion-induction of effector T lymphocytes by the chemokines IP10 and ***Mig*** .

L4 ANSWER 59 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN

TI Flexible programs of chemokine receptor expression on human polarized T helper 1 and 2 lymphocytes.

L4 ANSWER 60 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN

TI Expression of the ***CXCR3*** chemokine receptor and chemokines ***IP*** - ***10*** and ***MIG*** in RCC tissue.

L4 ANSWER 61 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN

TI Chemokine receptor expression on resident and inflammatory cells in the brain of macaques with Simian immunodeficiency virus encephalitis.

L4 ANSWER 62 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN

TI The chemokine receptors ***CXCR3*** and CCR5 mark subsets of T cells associated with certain inflammatory reactions.

L4 ANSWER 63 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN

TI ***Mig*** , the monokine induced by interferon-gamma, promotes tumor necrosis in vivo.

L4 ANSWER 64 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN

TI ***Mig*** and ***IP*** - ***10*** : CXC chemokines that target lymphocytes.

L4 ANSWER 65 OF 81 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN

TI Chemokine receptors and T cell chemotaxis.

L4 ANSWER 66 OF 81 CAPLUS COPYRIGHT 2005 ACS on STN

TI Cloning and characterization of the human ***CXCR3*** receptor

L4 ANSWER 67 OF 81 CAPLUS COPYRIGHT 2005 ACS on STN

TI CD8+ T cell-mediated skin disease in mice lacking IRF-2, the transcriptional attenuator of interferon-.alpha./beta. signaling

L4 ANSWER 68 OF 81 CAPLUS COPYRIGHT 2005 ACS on STN

TI Cutting edge: the T cell chemoattractant IFN-inducible protein 10 is essential in host defense against viral-induced neurologic disease

L4 ANSWER 69 OF 81 CAPLUS COPYRIGHT 2005 ACS on STN

TI Cutting edge: hierarchy of chemokine receptor and TCR signals regulating T cell migration and proliferation

L4 ANSWER 70 OF 81 CAPLUS COPYRIGHT 2005 ACS on STN

TI CD4+ T cell subsets during virus infection: protective capacity depends on effector cytokine secretion and on migratory capability

L4 ANSWER 71 OF 81 CAPLUS COPYRIGHT 2005 ACS on STN

TI Peroxisome proliferator-activated receptor-.gamma. activators inhibit IFN-.gamma.-induced expression of the T cell-active CXC chemokines ***IP*** - ***10*** , ***Mig*** , and I-TAC in human endothelial cells

L4 ANSWER 72 OF 81 CAPLUS COPYRIGHT 2005 ACS on STN

TI Expression of multiple functional chemokine receptors and monocyte chemoattractant protein-1 in human neurons

L4 ANSWER 73 OF 81 CAPLUS COPYRIGHT 2005 ACS on STN

TI The CXC chemokine H174 and methods for preventing damage to the nervous system

L4 ANSWER 74 OF 81 CAPLUS COPYRIGHT 2005 ACS on STN

TI Chemokine and chemokine receptor interactions provide a mechanism for selective T cell recruitment to specific liver compartments within hepatitis C-infected liver

L4 ANSWER 75 OF 81 CAPLUS COPYRIGHT 2005 ACS on STN

TI Switch in chemokine receptor expression upon TCR stimulation reveals novel homing potential for recently activated T cells

L4 ANSWER 76 OF 81 CAPLUS COPYRIGHT 2005 ACS on STN

TI Gene expression and production of the monokine induced by IFN-.gamma. (***MIG***), IFN-inducible T cell .alpha. chemoattractant (I-TAC), and IFN-.gamma.-inducible protein-10 (***IP*** - ***10***) chemokines by human neutrophils

L4 ANSWER 77 OF 81 CAPLUS COPYRIGHT 2005 ACS on STN

TI The T cell-specific CXC chemokines ***IP*** - ***10*** , ***Mig*** , and I-TAC are expressed by activated human bronchial epithelial cells

L4 ANSWER 78 OF 81 CAPLUS COPYRIGHT 2005 ACS on STN

TI Involvement of the ***IP*** - ***10*** chemokine in sarcoid granulomatous reactions

L4 ANSWER 79 OF 81 CAPLUS COPYRIGHT 2005 ACS on STN

TI Chemokine-binding protein A41L of poxvirus and its use as antiviral and anti-inflammatory

L4 ANSWER 80 OF 81 CAPLUS COPYRIGHT 2005 ACS on STN

TI Human CXC chemokine receptor 3, its cDNA sequence, and its diagnostic and therapeutic uses

L4 ANSWER 81 OF 81 CAPLUS COPYRIGHT 2005 ACS on STN

TI Differential expression of chemokine receptors and chemotactic responsiveness of type 1 T helper cells (Th1s) and Th2s

=> logoff

ALL L# QUERIES AND ANSWER SETS ARE DELETED AT LOGOFF

LOGOFF? (Y)/N/HOLD:hold

COST IN U.S. DOLLARS

SINCE FILE

TOTAL

ENTRY

SESSION

FULL ESTIMATED COST

28.96

29.59

SESSION WILL BE HELD FOR 60 MINUTES

STN INTERNATIONAL SESSION SUSPENDED AT 15:34:52 ON 07 JUN 2005

OM nucleic - nucleic search, using sw model

Run on: May 23, 2005, 11:57:45 ; Search time 7469 Seconds
(without alignments)
10834.143 Million cell updates/sec

Title: US-09-633-541-1
Perfect score: 1670
Sequence: 1 CCAACCACAAGCACCAAAGC.....TTTTTTTTTTTTTTTTTTTT 1670

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1670	100.0	1670	6	AR117009	AR117009 Sequence
2	1670	100.0	1670	6	BD195161	BD195161 CXCR3 che
3	1670	100.0	1670	6	AR456180	AR456180 Sequence
4	1623	97.2	1630	6	CQ868641	CQ868641 Sequence
5	1623	97.2	1670	6	AR380435	AR380435 Sequence
6	1623	97.2	1670	6	AX411189	AX411189 Sequence
7	1623	97.2	1670	6	AX548788	AX548788 Sequence
8	1623	97.2	1670	9	HSGPCRIN8	X95876 H.sapiens m
9	1612.4	96.6	1614	6	CQ834242	CQ834242 Sequence
10	1612	96.5	1625	6	CQ717993	CQ717993 Sequence
11	1589.4	95.2	1626	9	BC034403	BC034403 Homo sapi
12	1545.2	92.5	1703	6	AX805367	AX805367 Sequence
13	1545.2	92.5	1867	9	AF469635	AF469635 Homo sapi
14	1545.2	92.5	22608	6	CQ868640	CQ868640 Sequence
c 15	1545.2	92.5	248968	9	HSXDPB	AL590763 Homo sapi

Search completed: May 23, 2005, 15:35:04
Job time : 7481 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 23, 2005, 11:27:04 ; Search time 962 Seconds
(without alignments)
10276.474 Million cell updates/sec

Title: US-09-633-541-1
Perfect score: 1670
Sequence: 1 CCAACCACAAGCACCAAAGC.....TTTTTTTTTTTTTTTTTTT 1670

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1670	100.0	1670	2 AAV26557	Aav26557 Human IP-
2	1623	97.2	1630	13 ADR67007	Adr67007 Human can
3	1623	97.2	1670	6 ABN97338	Abn97338 Gene #383
4	1623	97.2	1670	8 ABZ42641	Abz42641 Human CXC
5	1623	97.2	1670	10 AAD58503	Aad58503 Human C-X
6	1623	97.2	1670	10 ADG33164	Adg33164 Human DNA
7	1623	97.2	1670	11 ADN39433	Adn39433 Cancer/an
8	1623	97.2	1670	11 ADI31654	Adi31654 Human cDN
9	1623	97.2	1670	12 ADH61809	Adh61809 Human G p
10	1623	97.2	1670	12 ADO29948	Ado29948 Human GPC
11	1623	97.2	1670	12 ADP10440	Adp10440 Reference
12	1623	97.2	1670	12 ADQ09120	Adq09120 Human CXC
13	1623	97.2	1670	13 ADR24759	Adr24759 Breast ca
14	1612.4	96.6	1614	12 ADQ95935	Adq95935 T cell ac
15	1545.2	92.5	1703	10 ADC46964	Adc46964 Human CXC

Search completed: May 23, 2005, 13:30:29
Job time : 974 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 23, 2005, 13:03:50 ; Search time 314 Seconds
(without alignments)
8702.491 Million cell updates/sec

Title: US-09-633-541-1
Perfect score: 1670
Sequence: 1 CCAACCACAAGCACCAAAGC.....TTTTTTTTTTTTTTTTTTTT 1670

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1670	100.0	1670	3	US-08-709-838-1	Sequence 1, Appli
2	1670	100.0	1670	3	US-08-829-839-1	Sequence 1, Appli
3	1670	100.0	1670	4	US-09-624-594-1	Sequence 1, Appli
4	1670	100.0	1670	4	US-09-607-156-1	Sequence 1, Appli
5	1623	97.2	1670	4	US-09-023-655-980	Sequence 980, App
6	1187.2	71.1	1293	4	US-09-016-434-1052	Sequence 1052, Ap
7	1107	66.3	1107	4	US-09-170-496D-19	Sequence 19, Appl
8	1105.4	66.2	1107	4	US-09-170-496D-173	Sequence 173, App
9	240	14.4	1679	1	US-08-202-056-6	Sequence 6, Appli
10	240	14.4	1679	1	US-08-076-093A-5	Sequence 5, Appli
11	240	14.4	1679	1	US-08-701-265-5	Sequence 5, Appli
12	240	14.4	1679	2	US-08-284-586-5	Sequence 5, Appli
13	240	14.4	1679	2	US-08-805-478-5	Sequence 5, Appli
14	240	14.4	1679	2	US-08-802-627A-5	Sequence 5, Appli
15	240	14.4	1679	2	US-08-801-238-5	Sequence 5, Appli

Search completed: May 23, 2005, 17:17:23
Job time : 322 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 23, 2005, 15:35:10 ; Search time 1051 Seconds
(without alignments)
9744.031 Million cell updates/sec

Title: US-09-633-541-1
Perfect score: 1670
Sequence: 1 CCAACCACAAGCACCAAAGC.....TTTTTTTTTTTTTTTTTTT 1670

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5695437 seqs, 3066160638 residues

Total number of hits satisfying chosen parameters: 11390874

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*

Search completed: May 23, 2005, 19:41:27
Job time : 1059 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 23, 2005, 13:14:22 ; Search time 6835 Seconds
(without alignments)
9974.321 Million cell updates/sec

Title: US-09-633-541-1
Perfect score: 1670
Sequence: 1 CCAACCACAAGCACCAAAGC.....TTTTTTTTTTTTTTTTTTT 1670

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 45554873 seqs, 20411521753 residues

Total number of hits satisfying chosen parameters: 91109746

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_Main:*

```

1: /cgn2_6/ptodata/1/pna/PCTUS1_COMB.seq:*
2: /cgn2_6/ptodata/1/pna/PCTUS2_COMB.seq:*
3: /cgn2_6/ptodata/1/pna/PCTUS_COMB.seq:*
4: /cgn2_6/ptodata/1/pna/US06_COMB.seq:*
5: /cgn2_6/ptodata/1/pna/US07_COMB.seq:*
6: /cgn2_6/ptodata/1/pna/US080_COMB.seq:*
7: /cgn2_6/ptodata/1/pna/US081_COMB.seq:*
8: /cgn2_6/ptodata/1/pna/US082_COMB.seq:*
9: /cgn2_6/ptodata/1/pna/US083_COMB.seq:*
10: /cgn2_6/ptodata/1/pna/US084_COMB.seq:*
11: /cgn2_6/ptodata/1/pna/US085_COMB.seq:*
12: /cgn2_6/ptodata/1/pna/US086_COMB.seq:*
13: /cgn2_6/ptodata/1/pna/US087_COMB.seq:*
14: /cgn2_6/ptodata/1/pna/US088_COMB.seq:*
15: /cgn2_6/ptodata/1/pna/US089_COMB.seq:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1670	100.0	1670	2	PCT-US04-31445-33	Sequence 33, Appl
2	1670	100.0	1670	28	US-09-633-541-1	Sequence 1, Appli
3	1670	100.0	1670	30	US-09-663-702-1	Sequence 1, Appli
4	1670	100.0	1670	30	US-09-663-799-1	Sequence 1, Appli
5	1670	100.0	1670	51	US-10-251-686-1	Sequence 1, Appli
6	1670	100.0	1670	66	US-10-949-135-33	Sequence 33, Appl
7	1670	100.0	1670	120	US-60-505-697-33	Sequence 33, Appl
8	1623	97.2	1630	49	US-10-170-235-27089	Sequence 27089, A
9	1623	97.2	1670	1	PCT-US02-18947-620	Sequence 620, App
10	1623	97.2	1670	1	PCT-US02-25766-2790	Sequence 2790, Ap
11	1623	97.2	1670	2	PCT-US03-01450-58	Sequence 58, Appl
12	1623	97.2	1670	2	PCT-US03-12946-449	Sequence 449, App
13	1623	97.2	1670	2	PCT-US03-13015-488	Sequence 488, App
14	1623	97.2	1670	2	PCT-US04-01100-620	Sequence 620, App
15	1623	97.2	1670	38	US-09-880-107-3833	Sequence 3833, Ap

OM protein - protein search, using sw model

Run on: May 20, 2005, 15:13:26 ; Search time 163 Seconds
(without alignments)
873.177 Million cell updates/sec

Title: US-09-633-541-2
Perfect score: 1907
Sequence: 1 MVLEVSDHQVLNDAEVAALL.....SSSRDSSWSETSEASYSGL 368

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1907	100.0	368	2	AAW54371	Aaw54371 Human IP-
2	1907	100.0	368	3	AAY90614	Aay90614 Human G p
3	1907	100.0	368	4	AAG80122	Aag80122 Human CXC
4	1907	100.0	368	6	ABP81795	Abp81795 Human CXC
5	1907	100.0	368	7	AAE38602	Aae38602 Human C-X
6	1907	100.0	368	7	ADC22539	Adc22539 Human G p
7	1907	100.0	368	7	ADF17988	Adf17988 Human CXC
8	1907	100.0	368	7	ADH14012	Adh14012 Human GPR
9	1907	100.0	368	7	ADN39434	Adn39434 Cancer/an
10	1907	100.0	368	8	ADH61810	Adh61810 Human G p
11	1907	100.0	368	8	ADO29458	Ado29458 Human GPC
12	1907	100.0	368	8	ADP12496	Adp12496 Protein e
13	1907	100.0	368	8	ADP12922	Adp12922 Protein e
14	1907	100.0	368	8	ADQ09119	Adq09119 Human CXC
15	1907	100.0	368	8	ADQ95936	Adq95936 T cell ac

Search completed: May 20, 2005, 15:56:45
Job time : 166 secs

OM protein - protein search, using sw model

Run on: May 20, 2005, 15:54:16 ; Search time 43 Seconds
(without alignments)
638.857 Million cell updates/sec

Title: US-09-633-541-2
Perfect score: 1907
Sequence: 1 MVLEVSDHQVLNDAEVAALL.....SSSRDSSWSETSEASYSGL 368

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1907	100.0	368	3	US-08-709-838-2
2	1907	100.0	368	3	US-08-829-839-2
3	1907	100.0	368	4	US-09-170-496D-20
4	1907	100.0	368	4	US-09-624-594-2
5	1907	100.0	368	4	US-09-607-156-2
6	1901	99.7	368	4	US-09-170-496D-174

Search completed: May 20, 2005, 16:02:10
Job time : 45 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 20, 2005, 15:59:47 ; Search time 136 Seconds
(without alignments)
905.138 Million cell updates/sec

Title: US-09-633-541-2
Perfect score: 1907
Sequence: 1 MVLEVSDHQVLNDAEVAALL.....SSSRDSSWSETSEASYSGL 368

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1434725 seqs, 334507595 residues

Total number of hits satisfying chosen parameters: 1434725

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA:*

```
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
```

RESULT 6

US-10-411-284-4

; Sequence 4, Application US/10411284

; Publication No. US20030224426A1

; GENERAL INFORMATION:

; APPLICANT: Li, Yi

; TITLE OF INVENTION: Human G-Protein Chemokine Receptor HSATU68

; FILE REFERENCE: PF218P1

; CURRENT APPLICATION NUMBER: US/10/411,284

; CURRENT FILING DATE: 2003-04-11

; PRIOR APPLICATION NUMBER: 60/371,725

; PRIOR FILING DATE: 2002-04-12

; PRIOR APPLICATION NUMBER: 09/101,518

; PRIOR FILING DATE: 1998-12-21

; PRIOR APPLICATION NUMBER: PCT/US96/00499

; PRIOR FILING DATE: 1996-01-11

; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: PatentIn Ver. 3.1

; SEQ ID NO 4

; LENGTH: 368

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-411-284-4

Query Match 100.0%; Score 1907; DB 15; Length 368;

Best Local Similarity 100.0%; Pred. No. 1.3e-167;

Matches 368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MVLEVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALY 60
         |||
Db      1 MVLEVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALY 60

Qy      61 SLLFLLGLLGN GAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLP LWA VDAAVQWVFG 120
         |||
Db      61 SLLFLLGLLGN GAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLP LWA VDAAVQWVFG 120

Qy      121 SGLCKVAGALFNINFYAGALLLACISFD RYLNIVHATQLYRRGPPARVTLTCLAVWGLCL 180
         |||
Db      121 SGLCKVAGALFNINFYAGALLLACISFD RYLNIVHATQLYRRGPPARVTLTCLAVWGLCL 180

Qy      181 LFALPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILA 240
         |||
Db      181 LFALPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILA 240
```



```

Qy      241 VLLVSRGQRRRLAMRLVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAK 300
      |||||||
Db      241 VLLVSRGQRRRLAMRLVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAK 300

Qy      301 SVTSGGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRDSSWSET 360
      |||||||
Db      301 SVTSGGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRDSSWSET 360

Qy      361 SEASYSGL 368
      |||||||
Db      361 SEASYSGL 368

```

Search completed: May 20, 2005, 16:12:41
Job time : 137 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 20, 2005, 15:56:57 ; Search time 483 Seconds
(without alignments)
889.910 Million cell updates/sec

Title: US-09-633-541-2
Perfect score: 1907
Sequence: 1 MVLEVSDHQVLNDAEVAALL.....SSSRDSSWSETSEASYSGL 368

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 6959266 seqs, 1168006243 residues

Total number of hits satisfying chosen parameters: 6959266

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_Main:*
1: /cgn2_6/ptodata/1/paa/PCTUS_COMB.pep:*
2: /cgn2_6/ptodata/1/paa/US06_COMB.pep:*
3: /cgn2_6/ptodata/1/paa/US07_COMB.pep:*
4: /cgn2_6/ptodata/1/paa/US080_COMB.pep:*
5: /cgn2_6/ptodata/1/paa/US081_COMB.pep:*
6: /cgn2_6/ptodata/1/paa/US082_COMB.pep:*
7: /cgn2_6/ptodata/1/paa/US083_COMB.pep:*
8: /cgn2_6/ptodata/1/paa/US084_COMB.pep:*
9: /cgn2_6/ptodata/1/paa/US085_COMB.pep:*
10: /cgn2_6/ptodata/1/paa/US086_COMB.pep:*
11: /cgn2_6/ptodata/1/paa/US087_COMB.pep:*
12: /cgn2_6/ptodata/1/paa/US088_COMB.pep:*
13: /cgn2_6/ptodata/1/paa/US089_COMB.pep:*
14: /cgn2_6/ptodata/1/paa/US090_COMB.pep:*
15: /cgn2_6/ptodata/1/paa/US091_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1907	100.0	368	1 PCT-US03-01450-59	Sequence 59, Appl

2	1907	100.0	368	1	PCT-US03-12946-2505	Sequence 2505, Ap
3	1907	100.0	368	1	PCT-US03-12946-2931	Sequence 2931, Ap
4	1907	100.0	368	1	PCT-US04-07930-2	Sequence 2, Appli
5	1907	100.0	368	1	PCT-US04-31445-34	Sequence 34, Appl
6	1907	100.0	368	1	PCT-US04-41506-122	Sequence 122, App
7	1907	100.0	368	20	US-09-633-541-2	Sequence 2, Appli
8	1907	100.0	368	20	US-09-663-702-2	Sequence 2, Appli
9	1907	100.0	368	20	US-09-663-799-2	Sequence 2, Appli
10	1907	100.0	368	27	US-10-170-205E-25225	Sequence 25225, A
11	1907	100.0	368	28	US-10-225-567A-74	Sequence 74, Appl
12	1907	100.0	368	28	US-10-239-423-78	Sequence 78, Appl
13	1907	100.0	368	28	US-10-251-385-20	Sequence 20, Appl
14	1907	100.0	368	28	US-10-251-686-2	Sequence 2, Appli
15	1907	100.0	368	28	US-10-295-027-752	Sequence 752, App

Search completed: May 20, 2005, 16:10:19
Job time : 485 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 20, 2005, 15:44:31 ; Search time 51 Seconds
(without alignments)
771.176 Million cell updates/sec

Title: US-09-633-541-2
Perfect score: 1907
Sequence: 1 MVLEVSDHQVLNDAEVAALL.....SSSRDSSWSETSEASYSGL 368

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 514143 seqs, 106874963 residues

Total number of hits satisfying chosen parameters: 514143

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New:*
1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*
2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/1/paa/US11_NEW_COMB.pep:*
8: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1907	100.0	368	1	PCT-US04-41506A-122
2	1907	100.0	368	6	US-10-920-055-6
3	1907	100.0	368	6	US-10-989-826-53
4	1907	100.0	368	7	US-11-021-951-155
5	1907	100.0	368	7	US-11-009-731A-122
6	1907	100.0	368	8	US-60-659-397-1246

7	1640.5	86.0	367	6	US-10-920-055-7	Sequence 7, Appli
8	640.5	33.6	371	7	US-11-021-951-154	Sequence 154, App
9	636.5	33.4	399	6	US-10-450-763-43968	Sequence 43968, A
10	635	33.3	372	6	US-10-989-826-22	Sequence 22, Appl
11	610	32.0	377	7	US-11-033-545-549	Sequence 549, App
12	606.5	31.8	350	7	US-11-033-545-305	Sequence 305, App
13	586	30.7	569	6	US-10-450-763-42732	Sequence 42732, A
14	576.5	30.2	352	7	US-11-021-951-189	Sequence 189, App
15	572.5	30.0	352	6	US-10-937-758A-37	Sequence 37, Appl

Search completed: May 20, 2005, 16:00:36
Job time : 53 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 20, 2005, 15:47:21 ; Search time 40 Seconds
(without alignments)
885.194 Million cell updates/sec

Title: US-09-633-541-2
Perfect score: 1907
Sequence: 1 MVLEVSDHQVLNDAEVAALL.....SSSRDSSWSETSEASYSGL 368

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1640.5	86.0	367	2 JE0349	interferon-inducib
2	641	33.6	374	2 S32785	G protein-coupled
3	640	33.6	374	2 S42628	G protein-coupled
4	635	33.3	372	2 S26667	G protein-coupled
5	633	33.2	360	2 A53611	interleukin-8 rece
6	631.5	33.1	327	2 S56162	MDCR15 protein - h
7	615.5	32.3	355	2 JQ1231	interleukin-8 rece
8	615	32.2	358	2 A53752	interleukin-8 rece
9	606.5	31.8	350	2 A39445	interleukin-8 rece
10	593.5	31.1	356	2 S42096	interleukin-8 rece
11	586	30.7	378	2 B55735	lymphocyte-specifi
12	582.5	30.5	352	2 G00048	fusin (LESTRA) - c
13	576.5	30.2	352	2 A45747	neuropeptide Y/pep
14	573	30.0	359	2 A48921	interleukin-8 rece
15	571	29.9	353	2 S28787	neuropeptide Y/pep